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## RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/918,508

TIME: 15:06:24

Input Set : A:\Q65478.app

Output Set: N:\CRF3\11142001\I918508.raw

3 <110> APPLICANT: KAKIMOTO, TATSUO  
 4 HIGUCHI, MASAYUKI  
 5 INOUE, TSUTOMU  
 7 <120> TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY  
 8 TO CYTOKININ RECEPTOR  
 10 <130> FILE REFERENCE: Q65478  
 12 <140> CURRENT APPLICATION NUMBER: 09/918,508  
 13 <141> CURRENT FILING DATE: 2001-08-01  
 15 <150> PRIOR APPLICATION NUMBER: JP 2001-073812  
 16 <151> PRIOR FILING DATE: 2001-03-15  
 18 <160> NUMBER OF SEQ ID NOS: 22  
 20 <170> SOFTWARE: PatentIn Ver. 2.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 3531  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Arabidopsis thaliana  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (1)..(3531)  
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34	1				5					10					15		
36	aag	tcg	tcg	agc	agt	gac	aag	aaa	tg	cta	aag	aag	cct	ctc	ttc	ttc	96
37	Lys	Ser	Ser	Ser	Ser	Asp	Lys	Lys	Trp	Leu	Lys	Lys	Pro	Leu	Phe	Phe	
38					20				25				30				
40	ctg	att	ttg	tgt	ggc	tct	ttg	gta	att	gtt	ttg	gtt	atg	ttc	tta	cgg	144
41	Leu	Ile	Leu	Cys	Gly	Ser	Leu	Val	Ile	Val	Leu	Val	Met	Phe	Leu	Arg	
42					35				40				45				
44	tta	ggt	aga	agt	cag	aag	gag	gag	aca	gat	tct	tgt	aat	gga	gaa	gag	192
45	Leu	Gly	Arg	Ser	Gln	Lys	Glu	Glu	Thr	Asp	Ser	Cys	Asn	Gly	Glu	Glu	
46		50					55			60							
48	aaa	gtg	ttg	tat	aga	cat	caa	aat	gtc	aca	aga	agt	gag	att	cat	gat	240
49	Lys	Val	Leu	Tyr	Arg	His	Gln	Asn	Val	Thr	Arg	Ser	Glu	Ile	His	Asp	
50	65					70				75					80		
52	ttg	gtc	tct	ttg	ttc	tct	gat	tca	gat	cag	gta	aca	tcc	ttt	gaa	tgt	288
53	Leu	Val	Ser	Leu	Phe	Ser	Asp	Ser	Asp	Gln	Val	Thr	Ser	Phe	Glu	Cys	
54					85				90				95				
56	cat	aag	gaa	tca	agc	cct	gga	atg	tg	aca	aac	tat	ggt	att	aca	tgt	336
57	His	Lys	Glu	Ser	Ser	Pro	Gly	Met	Trp	Thr	Asn	Tyr	Gly	Ile	Thr	Cys	
58					100				105				110				
60	tcc	ctg	agt	gtg	cgt	tct	gat	aaa	caa	gag	act	aga	ggg	ctt	ccc	tg	384
61	Ser	Leu	Ser	Val	Arg	Ser	Asp	Lys	Gln	Glu	Thr	Arg	Gly	Leu	Pro	Trp	
62					115				120				125				
64	aat	ctt	ggc	tta	gga	cat	tct	atc	tca	tca	aca	tct	tgt	atg	tgt	ggt	432
65	Asn	Leu	Gly	Leu	Gly	His	Ser	Ile	Ser	Ser	Thr	Ser	Cys	Met	Cys	Gly	
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70 145 150 155 160
72 cat gaa gaa ggg ctg gag cag ggt ttg tca tcg tat tta aga aat gca 528
73 His Glu Glu Gly Leu Glu Gln Gly Leu Ser Ser Tyr Leu Arg Asn Ala
74 165 170 175
76 tgg tgg tgt cta atc ctt ggt gtg tta gtg tgc cat aag att tat gta 576
77 Trp Trp Cys Leu Ile Leu Gly Val Leu Val Cys His Lys Ile Tyr Val
78 180 185 190
80 tct cat tct aaa gca cga ggt gag agg aaa gag aaa gta cat ctg caa 624
81 Ser His Ser Lys Ala Arg Gly Glu Arg Lys Glu Lys Val His Leu Gln
82 195 200 205
84 gag gct tta gct cca aag aag cag caa caa cgt gct cag act tct tct 672
85 Glu Ala Leu Ala Pro Lys Lys Gln Gln Gln Arg Ala Gln Thr Ser Ser
86 210 215 220
88 aga ggg gct gga aga tgg agg aag aat atc ctt ctc ctt ggt att tta 720
89 Arg Gly Ala Gly Arg Trp Arg Lys Asn Ile Leu Leu Leu Gly Ile Leu
90 225 230 235 240
92 gga gga gtt tcc ttc tct gtt tgg tgg ttt tgg gac act aat gag gag 768
93 Gly Gly Val Ser Phe Ser Val Trp Trp Phe Trp Asp Thr Asn Glu Glu
94 245 250 255
96 atc ata atg aaa agg agg gag act ttg gca aac atg tgt gac gaa cga 816
97 Ile Ile Met Lys Arg Arg Glu Thr Leu Ala Asn Met Cys Asp Glu Arg
98 260 265 270
100 gca cgt gtt tta caa gat cag ttc aat gtt agc ttg aac cat gtt cat 864
101 Ala Arg Val Leu Gln Asp Gln Phe Asn Val Ser Leu Asn His Val His
102 275 280 285
104 gcc ttg tct att ctt gta tct aca ttt cat cat ggt aaa atc cca tct 912
105 Ala Leu Ser Ile Leu Val Ser Thr Phe His His Gly Lys Ile Pro Ser
106 290 295 300
108 gcc att gat cag aga aca ttt gaa gaa tat act gag aga aca aac ttt 960
109 Ala Ile Asp Gln Arg Thr Phe Glu Glu Tyr Thr Glu Arg Thr Asn Phe
110 305 310 315 320
112 gag agg cca ctt act agt ggt gta gcg tat gct ttg aaa gtc cca cac 1008
113 Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala Leu Lys Val Pro His
114 325 330 335
116 tca gaa aga gag aaa ttt gaa aag gag cat gga tgg gca ata aag aaa 1056
117 Ser Glu Arg Glu Lys Phe Glu Lys Glu His Gly Trp Ala Ile Lys Lys
118 340 345 350
120 atg gaa act gag gac cag aca gtt gta caa gat tgt gtt cct gaa aac 1104
121 Met Glu Thr Glu Asp Gln Thr Val Val Gln Asp Cys Val Pro Glu Asn
122 355 360 365
124 ttt gat ccc gca ccg att caa gac gaa tac gcg cca gtt ata ttt gct 1152
125 Phe Asp Pro Ala Pro Ile Gln Asp Glu Tyr Ala Pro Val Ile Phe Ala
126 370 375 380
128 caa gaa act gtt tcc cat att gta tcg gtc gac atg atg tct gga gaa 1200
129 Gln Glu Thr Val Ser His Ile Val Ser Val Asp Met Met Ser Gly Glu
130 385 390 395 400
132 gaa gac cgt gaa aac atc tta cgg gca agg gca tca gga aaa gga gtg 1248

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137	Leu	Thr	Ser	Pro	Phe	Lys	Leu	Leu	Lys	Ser	Asn	His	Leu	Gly	Val	Val	
138				420					425					430			
140	ttg	acc	ttt	gct	gtc	tat	gac	acg	agc	cta	ccg	cct	gat	gct	aca	gaa	1344
141	Leu	Thr	Phe	Ala	Val	Tyr	Asp	Thr	Ser	Leu	Pro	Pro	Asp	Ala	Thr	Glu	
142			435					440					445				
144	gaa	cag	cgt	gtt	gaa	gca	act	att	ggg	tac	ctt	ggt	gca	tca	tat	gat	1392
145	Glu	Gln	Arg	Val	Glu	Ala	Thr	Ile	Gly	Tyr	Leu	Gly	Ala	Ser	Tyr	Asp	
146		450					455					460					
148	atg	cca	tcg	ctg	gtg	gag	aaa	ctt	ctt	cac	caa	ctt	gcc	agc	aaa	cag	1440
149	Met	Pro	Ser	Leu	Val	Glu	Lys	Leu	Leu	His	Gln	Leu	Ala	Ser	Lys	Gln	
150	465					470				475					480		
152	aca	att	gct	gtg	gat	gtt	tac	gac	aca	act	aac	act	tca	ggt	cta	ata	1488
153	Thr	Ile	Ala	Val	Asp	Val	Tyr	Asp	Thr	Thr	Asn	Thr	Ser	Gly	Leu	Ile	
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156	aaa	atg	tat	ggc	tca	gaa	att	ggg	gat	ata	agt	gag	cag	cat	ata	agt	1536
157	Lys	Met	Tyr	Gly	Ser	Glu	Ile	Gly	Asp	Ile	Ser	Glu	Gln	His	Ile	Ser	
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161	Ser	Leu	Asp	Phe	Gly	Asp	Pro	Ser	Arg	Asn	His	Glu	Met	His	Cys	Arg	
162			515					520					525				
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165	Phe	Lys	His	Lys	Leu	Pro	Ile	Pro	Trp	Thr	Ala	Ile	Thr	Pro	Ser	Ile	
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173	Ile	Asn	Arg	Ile	Ala	Thr	Val	Glu	Glu	Asp	Cys	Gln	Lys	Met	Arg	Glu	
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177	Leu	Lys	Ala	Arg	Ala	Glu	Ala	Ala	Asp	Ile	Ala	Lys	Ser	Gln	Phe	Leu	
178			580					585					590				
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181	Ala	Thr	Val	Ser	His	Glu	Ile	Arg	Thr	Pro	Met	Asn	Gly	Val	Leu	Gly	
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186		610					615					620					
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189	Tyr	Ala	Gln	Thr	Ala	His	Gly	Ser	Gly	Lys	Asp	Leu	Thr	Ser	Leu	Ile	
190	625				630					635					640		
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193	Asn	Glu	Val	Leu	Asp	Gln	Ala	Lys	Ile	Glu	Ser	Gly	Arg	Leu	Glu	Leu	
194				645					650					655			
196	gaa	aat	gtg	cct	ttt	gat	atg	cgt	ttt	att	ctt	gat	aat	gtt	tca	tct	2016
197	Glu	Asn	Val	Pro	Phe	Asp	Met	Arg	Phe	Ile	Leu	Asp	Asn	Val	Ser	Ser	

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204	gtt tct agt	caa gtt cct	gat gtt gta gtc	ggt gat ccg agt	cgg ttc	2112		
205	Val Ser Ser	Gln Val Pro	Asp Val Val Val	Gly Asp Pro Ser	Arg Phe			
206		690		695		700		
208	cgg cag atc	att aca aac	ctg gtt gga aac	tca atc aaa ttc	aca cag	2160		
209	Arg Gln Ile	Ile Thr Asn	Leu Val Gly Asn	Ser Ile Lys Phe	Thr Gln			
210	705		710		715		720	
212	gaa agg gga	cac ata ttt	atc tca gtg cac	ctt gca gat gag	gta aag	2208		
213	Glu Arg Gly	His Ile Phe	Ile Ser Val His	Leu Ala Asp	Glu Val Lys			
214		725		730		735		
216	gag cct ctt	act att gaa	gac gca gtg	cta aaa cag	cga cta gct	tta	2256	
217	Glu Pro Leu	Thr Ile Glu	Asp Ala Val	Leu Lys Gln	Arg Leu Ala	Leu		
218		740		745		750		
220	gga tgc agc	gag tcc ggt	gag aca gtt	agc ggg ttt	cct gcg gta	aat	2304	
221	Gly Cys Ser	Glu Ser Gly	Glu Thr Val	Ser Gly Phe	Pro Ala Val	Asn		
222		755		760		765		
224	gca tgg gga	agc tgg aag	aat ttc aag	aca tgt tac	agt act gag	agt	2352	
225	Ala Trp Gly	Ser Trp Lys	Asn Phe Lys	Thr Cys Tyr	Ser Thr Glu	Ser		
226		770		775		780		
228	cag aat tct	gat caa atc	aaa ttg cta	gtt aca gtg	gag gac act	gga	2400	
229	Gln Asn Ser	Asp Gln Ile	Lys Leu Leu	Val Thr Val	Glu Asp Thr	Gly		
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232	gtt ggc ata	cct gtg gat	gca caa ggc	cga atc ttc	aca cct ttt	atg	2448	
233	Val Gly Ile	Pro Val Asp	Ala Gln Gly	Arg Ile Phe	Thr Pro Phe	Met		
234		805		810		815		
236	caa gcc gac	agt tcc aca	tcg cgg act	tat ggt gga	act ggc ata	ggt	2496	
237	Gln Ala Asp	Ser Ser Thr	Ser Arg Thr	Tyr Gly Gly	Thr Gly Ile	Gly		
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240	ttg agt ata	agc aaa cgt	ttg gtt gaa	ctc atg caa	gga gag atg	ggg	2544	
241	Leu Ser Ile	Ser Lys Arg	Leu Val Glu	Leu Met Gln	Gly Glu Met	Gly		
242		835		840		845		
244	ttt gtg agt	gag ccc ggg	ata ggc agt	act ttt tca	ttt act gga	gtt	2592	
245	Phe Val Ser	Glu Pro Gly	Ile Gly Ser	Thr Phe Ser	Phe Thr Gly	Val		
246		850		855		860		
248	ttc ggg aaa	gca gaa aca	aat acg tcg	att act aag	ctg gaa cga	ttc	2640	
249	Phe Gly Lys	Ala Glu Thr	Asn Thr Ser	Ile Thr Lys	Leu Glu Arg	Phe		
250	865		870		875		880	
252	gat cta gct	att cag gag	ttt aca gga	ttg aga gca	tta gtt att	gat	2688	
253	Asp Leu Ala	Ile Gln Glu	Phe Thr Gly	Leu Arg Ala	Leu Val Ile	Asp		
254		885		890		895		
256	aac aga aac	att aga gca	gag gtc acc	agg tac gaa	ctt cgg aga	ctg	2736	
257	Asn Arg Asn	Ile Arg Ala	Glu Val Thr	Arg Tyr Glu	Leu Arg Arg	Leu		
258		900		905		910		
260	gga ata tct	gca gac att	gtt tca agt	ctg aga atg	gca tgc act	tgt	2784	
261	Gly Ile Ser	Ala Asp Ile	Val Ser Ser	Leu Arg Met	Ala Cys Thr	Cys		
262		915		920		925		

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268 gcc tgg aac aag gaa gaa ttt tca gta ctt gac gag ttg ttt acc cga 2880
269 Ala Trp Asn Lys Glu Phe Ser Val Leu Asp Glu Leu Phe Thr Arg
270 945 950 955 960
272 agc aaa gta acc ttt aca aga gtc cca aag att ttt ctt ttg gca act 2928
273 Ser Lys Val Thr Phe Thr Arg Val Pro Lys Ile Phe Leu Leu Ala Thr
274 965 970 975
276 tct gca act ctt act gag cgc agt gag atg aag tct act ggt ctc atc 2976
277 Ser Ala Thr Leu Thr Glu Arg Ser Glu Met Lys Ser Thr Gly Leu Ile
278 980 985 990
280 gat gag gtg gtg ata aag cct ctt cgg atg agt gtc tta ata tgt tgc 3024
281 Asp Glu Val Val Ile Lys Pro Leu Arg Met Ser Val Leu Ile Cys Cys
282 995 1000 1005
284 ttg caa gaa acc ctt gtc aat ggc aag aag agg caa ccg aac aga cag 3072
285 Leu Gln Glu Thr Leu Val Asn Gly Lys Lys Arg Gln Pro Asn Arg Gln
286 1010 1015 1020
288 cga aga aat ctt gga cac ttg cta aga gaa aaa cag att ctg gtt gtg 3120
289 Arg Arg Asn Leu Gly His Leu Leu Arg Glu Lys Gln Ile Leu Val Val
290 1025 1030 1035 1040
292 gat gat aat ctt gtg aac aga cga gtt gca gaa ggt gca ctt aag aaa 3168
293 Asp Asp Asn Leu Val Asn Arg Arg Val Ala Glu Gly Ala Leu Lys Lys
294 1045 1050 1055
296 tat gga gct att gtt aca tgc gtt gag agt ggc aaa gct gca ttg gca 3216
297 Tyr Gly Ala Ile Val Thr Cys Val Glu Ser Gly Lys Ala Ala Leu Ala
298 1060 1065 1070
300 atg ctt aag ccg cct cat aac ttc gat gct tgc ttc atg gat ctc cag 3264
301 Met Leu Lys Pro Pro His Asn Phe Asp Ala Cys Phe Met Asp Leu Gln
302 1075 1080 1085
304 atg cct gaa atg gat gga ttt gaa gcg aca agg aga gtc cgt gag ctg 3312
305 Met Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Val Arg Glu Leu
306 1090 1095 1100
308 gag agg gaa atc aat aag aaa ata gct tct gga gaa gtt tca gct gaa 3360
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310 1105 1110 1115 1120
312 atg ttc tgt aaa ttt agt agt tgg cac gtc ccg ata tta gca atg aca 3408
313 Met Phe Cys Lys Phe Ser Ser Trp His Val Pro Ile Leu Ala Met Thr
314 1125 1130 1135
316 gca gat gtt att cag gct act cat gaa gaa tgc atg aaa tgt gga atg 3456
317 Ala Asp Val Ile Gln Ala Thr His Glu Glu Cys Met Lys Cys Gly Met
318 1140 1145 1150
320 gat ggt tat gta tca aaa ccg ttt gaa gag gaa gtg ctc tac aca gcg 3504
321 Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Val Leu Tyr Thr Ala
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